



- <110> MCKERRACHER, LISA LASKO, DANA
- <120> CLOSTRIDIUM BOTULINUM C3 EXOTRANSFERASE COMPOSITIONS AND METHODS FOR TREATING TUMOUR SPREADING
- <130> 1912-0330PUS1
- <140> US 10/573,658
- <141> 2006-03-28
- <150> PCT/CA04/01763
- <151> 2004-09-29
- <150> US 10/902,879
- <151> 2004-08-02
- <150> US 60/506,162
- <151> 2003-09-29
- <160> 59
- <170> PatentIn version 3.1
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- <213> Artificial Sequence
- <220>
- <223> Oligonucleotide used to remove the stop codon from ADP-ribosyl
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aat tt: Asn Le				_	-		-				-	288	
aag ac Lys Th												336	
tta gga Leu Gl		_										384	
aat aaa Asn Ly: 13	s Thr											432	
aga ct Arg Le												480	
ttt gca Phe Ala		-						_	_			528	
aag gca Lys Ala												576	

atg ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu 195 200 205	624
tct tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr 210 215 220	672
gct atc aat cct aaa gaa ttc gtg atg gaa tcc cgc aaa cgc gca agg Ala Ile Asn Pro Lys Glu Phe Val Met Glu Ser Arg Lys Arg Ala Arg 225 230 235 240	720
cag aca tac acc cgg tac cag act cta gag cta gag aag gag ttt cac Gln Thr Tyr Thr Arg Tyr Gln Thr Leu Glu Leu Glu Lys Glu Phe His 245 250 255	768
ttc aat cgc tac ttg acc cgt cgg cga agg atc gag atc gcc cac gcc Phe Asn Arg Tyr Leu Thr Arg Arg Arg Ile Glu Ile Ala His Ala 260 265 270	816
ctg tgc ctc acg gag cgc cag ata aag att tgg ttc cag aat cgg cgc Leu Cys Leu Thr Glu Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg 275 280 285	864
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Met Lys Trp Lys Lys Glu Asn

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<220 <223		Seque (Clos													С3	
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		tct Ser														-10
		gct Ala														96
		gct Ala 35														144
		aaa Lys														192
		aag Lys														240
		ata Ile			_	_			_							288
_		cct Pro	_			_			_		-	-		-		336
		aca Thr 115	_													384
		acg Thr														432
		gaa Glu														480

ttt gca gga aga Phe Ala Gly Arg				e Lys Val	-		
aag gca gga tat Lys Ala Gly Tyr 180							
atg ttg ctt cct Met Leu Leu Pro 195							
tct tct gat ggt Ser Ser Asp Gly 210					Met Met		
gct atc aat cct Ala Ile Asn Pro 225							า
cgt cgc atg aag Arg Arg Met Lys			_	r Ser Gly	-		
gac tga Asp							774
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-				P-ribosyl ennapedia			
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Gly Ser Ser Arg	5		10		_	15	
Gly Ser Ser Arg 1 Gln Lys Ala Tyr	Ser Asn	Thr Tyr	Gln Gl 25	u Phe Thr	Asn Ile	15 Asp Glr	า

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser 70 Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met 95 Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr 105 100 Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile 120 Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp 135 140 130 Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln 155 150 Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser 170 165 Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu 185 180 Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu 200 205 195 Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr 215 210

Ala Ile Asn Pro Lys Glu Phe Arg Gln Ile Lys Ile Trp Phe Gln Asn 225 230 235 240

Arg Arg Met Lys Trp Lys Lys Val Asp Ser Ser Gly Arg Ile Val Thr 245 250 255

Asp

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	10 54 DNA Artificial Sequence	
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<210><211><211><212><212><213>	11 26 DNA Artificial Sequence	
<220> <223>	Oligonucleotide used inthe amplification of a sequence corresponding to amino acid 27-72 of HIV-1 Tat	

gaatco	caago	at	:cca	ggaa	ig to	agco										26
<210>	12															
<211>																
<212>		Ą														
<213>		_	icia	l Se	quen	ıce										
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<223>												of a		queno	ce	
<400>	12															
accago		c ac	cctt	ctga	ıt a											21
_				-												
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<220>				<u> </u>				_1 _	71 FO FO			_			G2	
<223>												trar quenc		case	C3	
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<222>	(1)		(876	;)												
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gga t																48
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1				5					10					15		
caa a	ag go	ct t	tat	tca	aat	act	tac	cag	gag	ttt	act	aat	att	gat	caa	96
Gln L								_						_		
•			20				•	25					30			
gca a	aa go	ct t	tgg	ggt	aat	gct	cag	tat	aaa	aag	tat	gga	cta	agc	aaa	144
Ála L																
	3	5					40					45				
tca g	aa aa	aa q	gaa	gct	ata	gta	tca	tat	act	aaa	agc	gct	agt	gaa	ata	192
Ser G											Ser					
5	0					55					60					
aat g	ga aa	ag (cta	aga	caa	aat	aag	gga	gtt	atc	aat	gga	ttt	cct	tca	240
Asn G																
65	- •			-	70		-	-		75		-			80	
aat t	ta a	ta a	aaa	caa	att	qaa	ctt	tta	gat	aaa	tct	ttt	aat	aaa	atq	288
Asn L																
			-	85					90	-				95		
aag a																336

Lys	Thr	Pro	Glu 100	Asn	Ile	Met	Leu	Phe 105	Arg	Gly	Asp	Asp	Pro 110	Ala	Tyr	
			gaa Glu													384
		_	gct Ala		-	_	_		_	_					_	432
			tat Tyr								-		_			480
			aga Arg								_	_				528
			tat Tyr 180													576
_	_		cct Pro	_		-					_	_	_	_	_	624
			ggt Gly							_		_	_			672
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Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys 35 40 45

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile 50 55 60

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser 65 70 75 80

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met 85 90 95

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr 100 105 110

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile 115 120 125

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp 130 135 140

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln 145 150 155 160

Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser 165 170 175

Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu 180 185 190

Met Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu 195 200 205 Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr 215 Ala Ile Asn Pro Lys Glu Phe Lys His Pro Gly Ser Gln Pro Lys Thr 225 230 235 Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His Cys Gln Val 250 Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly Arg Lys Arg Arg 260 265 270 Gln Arg Arg Arg Ala His Gln Asn Ser Gln Thr His Gln Ala Ser Leu 285 Ser Lys Gln 290 <210> 15 <211> 39 <212> DNA <213> Artificial Sequence <220> <223> Oligonucleotide used in the cloning of sequences from HIV-1 <400> 15 39 aattctatgg tcgtaaaaaa cgtcgtcaac gtcgtcgtg <210> 16 <211> 39 <212> DNA <213> Artificial Sequence <220> <223> Oligonucleotide used in the cloning of sequences from HIV-1 Tat <400> 16 39 gataccagca ttttttgcag cagttgcagc agcacagct <210> 17 <211> 756 <212> DNA <213> Artificial Sequence <220> <223> Sequence of C3-TS: Includes ADP-ribosyl transferase C3

(Clostridium botulinum) and HIV-1 Tat sequence.

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-		-			aat Asn	_	_			-						144
	_		_	_	ata Ile	_					_	_	-	-		192
		_		-	caa Gln 70		_		_							240
					gtt Val	-			-							288
-			-		att Ile	_			_		_					336
			-		caa Gln											384
					gaa Glu											432
					tat Tyr 150											480
	_		-		att Ile						-	_				528
_	_				gac Asp			_	_		-				-	576
atg	ttg	ctt	cct	aga	cat	agt	act	tat	cat	ata	gac	gat	atg	aga	ttg	624

Met Leu Leu 195	Pro Arg His	Ser Thr Tyr 200	His Ile Asp	Asp Met Arg 205	Leu
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-	_	Phe Tyr Gly	gct aaa aaa Ala Lys Lys 235		_
		ggc ccg cat Gly Pro His			756
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Gln Lys Ala	Tyr Ser Asn 20	Thr Tyr Gln 25	Glu Phe Thr	Asn Ile Asp 30	Gln
Ala Lys Ala 35	Trp Gly Asn	Ala Gln Tyr 40	Lys Lys Tyr	Gly Leu Ser 45	Lys
Ser Glu Lys 50	Glu Ala Ile	Val Ser Tyr 55	Thr Lys Ser	Ala Ser Glu	Ile
Asn Gly Lys 65	Leu Arg Gln 70	Asn Lys Gly	Val Ile Asn 75	Gly Phe Pro	Ser 80
Asn Leu Ile	Lys Gln Val 85	Glu Leu Leu	Asp Lys Ser	Phe Asn Lys 95	Met
Lys Thr Pro	Glu Asn Ile 100	Met Leu Phe 105	Arg Gly Asp	Asp Pro Ala	Tyr
Leu Gly Thr 115		Asn Thr Leu 120	Leu Asn Ser	Asn Gly Thr 125	Ile

130 135 140 Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln 145 150 Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser 165 170 Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu 180 185 Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu 195 200 205 Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr 215 Ala Ile Asn Pro Lys Glu Phe Tyr Gly Ala Lys Lys Arg Arg Gln Arg 225 230 235 Arg Arg Val Asp Ser Ser Gly Pro His Arg Asp 245 <210> 19 <211> 1413 <212> DNA <213> Artificial Sequence <220> <223> Includes GST sequences, ADP-ribosyl transferase C3 (C. botulinum) sequence and a random basic amino acid sequence. <220> <221> CDS <222> (1)..(1413) <400> 19 atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc 48 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro 10 15 5 act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg 96 Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu 30

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp

25

					ggt Gly											14	· 4
	-				aat Asn						-		_	_		19)2
		_		_	gcc Ala 70											24	0
					cca Pro											28	8 8
		_	_	-	att Ile											33	36
	-		-		ctc Leu		-	_			_	_			_	38	3 4
_	-				gaa Glu											43	32
	_		-		cat His 150		_		_	_		-	_		-	48	30
-	-				gac Asp											52	28
_	-				cgt Arg		-	-					-	_		57	76
					tat Tyr											62	24
_					gac Asp					_	_	_	_	_		67	12
					gac Asp 230											72	20
					aat Asn											76	58
gca	aaa	gct	tgg	ggt	aat	gct	cag	tat	aaa	aag	tat	gga	cta	agc	aaa	81	L 6

Ala	Lys	Ala	Trp 260	Gly	Asn	Ala	Gln	Tyr 265	Lys	Lys	Tyr	Gly	Leu 270	Ser	Lys	
							tca Ser 280									864
		_		-			aag Lys		_							912
					_	-	ctt Leu		-						-	960
-			_			-	tta Leu		_		-	_		_		1008
			-				act Thr									1056
		_	_		_	-	gct Ala 360		_	_					_	1104
							agt Ser									1152
	_		_				aca Thr				_	_				1200
							att Ile									1248
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<223> Includes GST sequences, ADP-ribosyl transferase C3
 (C. botulinum) sequence and a random basic amino acid
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Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu 20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys 50 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser 100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn 130 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr 180 185 190 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr 435 440 Ala Ile Asn Pro Lys Glu Phe Arg Arg Lys Gln Arg Arg Lys Arg Arg 450 455 Leu Gln Ala Ala Ser 465 <210> 21 <211> 16 <212> PRT <213> Artificial Sequence <220> <223> Random basic amino acid sequence of C3Basic1 <400> 21 Lys Arg Arg Arg Arg Pro Lys Lys Arg Arg Arg Ala Lys Arg Arg 5 <210> 22 <211> 48 <212> DNA <213> Artificial Sequence <220> <223> Oligonucleotide used in the cloning of a random basic amino acid sequence in C3Basic1 <400> 22 48 aagagaaggc gaagaagacc taagaagaga cgaagggcga agaggaga <210> 23 <211> 48 <212> DNA <213> Artificial Sequence <223> Oligonucleotide used in the cloning of a random basic amino acid sequence in C3Basic1 <400> 23 48 ttctcttccg cttcttctgg attcttctct gcttcccgct tctcctct

Met Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu

425

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gca aaa gct tgg ggt aat gct cag tat aaa aag tat gga cta agc aaa Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys 35 40 45	44
tca gaa aaa gaa gct ata gta tca tat act aaa agc gct agt gaa ata	92
Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile 50 . 60	
aat gga aag cta aga caa aat aag gga gtt atc aat gga ttt cct tca Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser 65 70 75 80	40
aat tta ata aaa caa gtt gaa ctt tta gat aaa tct ttt aat aaa atg Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met 85 90 95	88
aag acc cct gaa aat att atg tta ttt aga ggc gac gac cct gct tat Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr 100 105 110	36
tta gga aca gaa ttt caa aac act ctt ctt aat tca aat ggt aca att Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile 115 120 125	84
aat aaa acg gct ttt gaa aag gct aaa gct aag ttt tta aat aaa gat Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp 130 135 140	32
aga ctt gaa tat gga tat att agt act tca tta atg aat gtt tct caa Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln 145 150 155 160	80

ttt gca gga aga cca att att aca aaa ttt aaa gta gca aaa ggc tca Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser 165 170 175	528
aag gca gga tat att gac cct att agt gct ttt cag gga caa ctt gaa	576
Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu 180 185 190	
atg ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu 195 200 205	624
tct tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr 210 215 220	672
gct atc aat cct aaa gaa ttc aag aga agg cga aga aga cct aag aag Ala Ile Asn Pro Lys Glu Phe Lys Arg Arg Arg Arg Pro Lys Lys 225 230 235 240	720
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agc ggc cgc atc gtg act gac tga Ser Gly Arg Ile Val Thr Asp 260	792
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Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile 50 55 60	

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser 70 75 Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met 90 Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr 105 Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile 115 Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp 130 140 Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln 150 Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser 170 165 Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu 180 185 Met Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu 195 200 Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr 220 210 215 Ala Ile Asn Pro Lys Glu Phe Lys Arg Arg Arg Arg Pro Lys Lys 225 230 235 Arg Arg Arg Ala Lys Arg Arg His His His His His Val Asp Ser 250 245 Ser Gly Arg Ile Val Thr Asp 260 <210> 26

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_			-			_	tta Leu		_		-					336
			-				act Thr 120									384
		_	_		-	-	gct Ala		_	-					_	432
_		-					agt Ser				_		_			480
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_				_		_	act Thr 200				_	_	_	_	_	624
		-					ata Ile			_			-	J .,		672
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Gln	Lys	Ala	Tyr 20	Ser	Asn	Thr	Tyr	Gln 25	Glu	Phe	Thr	Asn	Ile 30	Asp	Gln	
Ala	Lys	Ala 35	Trp	Gly	Asn	Ala	Gln 40	Tÿr	Lys	Lys	Tyr	Gly 45	Leu	Ser	Lys	
Ser	Glu 50	Lys	Glu	Ala	Ile	Val 55	Ser	Tyr	Thr	Lys	Ser 60	Ala	Ser	Glu	Ile	
Asn 65	Gly	Lys	Leu	Arg	Gln 70	Asn	Lys	Gly	Val	Ile 75	Asn	Gly	Phe	Pro	Ser 80	
Asn	Leu	Ile	Lys	Gln 85	Val	Glu	Leu	Leu	Asp 90	Lys	Ser	Phe	Asn	Lys 95	Met	
Lys	Thr	Pro	Glu 100	Asn	Ile	Met	Leu	Phe 105	Arg	Gly	Asp	Asp	Pro 110	Ala	Tyr	
Leu	Gly	Thr 115	Glu	Phe	Gln	Asn	Thr 120	Leu	Leu	Asn	Ser	Asn 125	Gly	Thr	Ile	
Asn	Lys 130	Thr	Ala	Phe	Glu	Lys 135	Ala	Lys	Ala	Lys	Phe 140	Leu	Asn	Lys	Asp	

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln 145 150 155 Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser 165 170 175 Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu 185 180 Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu 200 Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr 215 220 Ala Ile Asn Pro Lys Glu Phe Lys Arg Arg Arg Arg Lys Lys Arg Arg 225 . 230 235 240 Gln Arg Arg His His His His His Val Asp Ser Ser Gly Arg 245 250 Ile Val Thr Asp 260 <210> 31 <211> 9 <212> PRT <213> Artificial Sequence <220> <223> Reverse HIV-1 Tat amino acid sequence of C3Basic3 <400> 31 Arg Arg Lys Gln Arg Arg Lys Arg Arg <210> 32 <211> 27 <212> DNA <213> Artificial Sequence <220> <223> Oligonucleotide used in the cloning of a reverse HIV Tat sequence in C3Basic3

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	a aaa gaa u Lys Gli						er Ala				192				
	a aag cta y Lys Le				Val 1						240				
	a ata aa u Ile Ly		_		-						288				
	cc cct gad ir Pro Gli										336				

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245 250 255

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gca aa Ala Ly															144
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aat tt Asn Le				-	-			-						-	288
aag ac Lys Th															336
tta gg Leu Gl		_													384
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aga ct Arg Le	_					-				_		_			480

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aag gca gga tat att gac cct att agt gct ttt gca gga caa ctt gaa Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu 180 185 190	576
atg ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg Met Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu 195 200 205	624
tct tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr 210 215 220	672
gct atc aat cct aaa gaa ttc gtg atg aat ccc gca aac gcg caa ggc Ala Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly 225 230 235 240	720
aga cat aca ccc ggt acc aga ctc tag agctagagaa ggagtttcac Arg His Thr Pro Gly Thr Arg Leu 245	767
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Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile 50 55 60	

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser 70 75 65 Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met 90 Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr 100 105 Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile 120 Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp 130 135 140 Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln 145 150 155 Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser 165 170 175 Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu 180 185 Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu 195 200 Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr 210 215 220

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_	_						_	gag Glu 25					_			96
	_				_	_		aaa Lys	_							144
								act Thr								192
								gtt Val								240
				-	-			gat Asp						_	_	288
		-			_			aga Arg 105		-	-		-			336
		_						ctt Leu								384
								gct Ala								432
	_					_		tca Ser				_				480
-		_						ttt Phe		-	_				_	528
-				_			-	gct Ala 185		_				_	_	576
_			_		_			cat His		-	_	_	_	_		624
tct	gat	ggt	aaa	caa	ata	ata	att	aca	gca	aca	atg	atg	ggc	aca	gct	672

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cat aca ccc ggt His Thr Pro Gly		ag agctagagaa g	gagtttcac ttcaa	teget 774
acttgacccg tcgg	cgaagg atcgaga	tcg cccacgccct	gtgcctcacg gagc	gccaga 834
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Lys Ala Tyr Ser 20	Asn Thr Tyr G	ln Glu Phe Thr 25	Asn Ile Asp Gln 30	Ala
Lys Ala Trp Gly 35	Asn Ala Gln T		Gly Leu Ser Lys 45	Ser
Glu Lys Glu Ala 50	Ile Val Ser T	-	Ala Ser Glu Ile 60	Asn
Gly Lys Leu Arg 65	Gln Asn Lys G	ly Val Ile Asn 75	Gly Phe Pro Ser	Asn 80
Leu Ile Lys Gln	Val Glu Leu Leu Leu Leu Leu Leu Leu Leu Leu Le	eu Asp Lys Ser 90	Phe Asn Lys Met 95	Lys
Thr Pro Glu Asn		he Arg Gly Asp	Asp Pro Ala Tyr 110	Leu

Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile Asn 120 125 115 Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp Arg 135 130 Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln Phe 150 155 Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser Lys 165 170 Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met 180 185 Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser 200 Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala 210 215 Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 His Thr Pro Gly Thr Arg Leu

245

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                                                        15
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Lys Lys Cys Cys Phe His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu
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                                                    30
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Gly Ile Ser Tyr Gly Arg Lys Arg Arg Gln Arg Arg Arg Ala His Gln
        35
                           40
Asn Ser Gln Thr His Gln Ala Ser Leu Ser Lys Gln
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<400> 47

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                            40
Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile Asn
                                             60
                        55
Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser Asn
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                    70
Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met Lys
                                     90
Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr Leu
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            100
Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile Asn
                                                 125
                            120
        115
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                        135
Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln Phe
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Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser Lys
                                     170
                165
Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Ala Leu Glu Met
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                                185
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Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala
                                             220
                        215
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                    230
His Thr Pro Gly Thr Arg Leu
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245

120

180 240

300

360

480

540

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720

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                                                                        120
                                                                        180
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